

Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1. (Currently Amended) A method for making transplants resistant to BNYVV by introducing Method for inducing resistance to a group I virus comprising a TGB2 sequence in a plant cell or a plant, comprising the following steps of:

- preparing a nucleotide construct to express a TGB2 protein whose functional activity has been changed, the construct comprising a nucleotide sequence having at least 70% homology with homologous to the nucleotide sequence of SEQ ID NO: 1 or its complement or its corresponding RNA sequence, the sequence including at least one nucleotide deletion, insertion or substitution which results in a mutant TGB2 protein being expressed which has at least one amino acid change compared to wild-type TGB2; said sequence TGB2 of said virus or its complementary cDNA, being operably linked to one or more regulatory sequence(s) active in a plant,

- transforming a plant cell with the nucleotide construct, and possibly

- regenerating a transgenic plant from the transformed plant cell wherein said transgenic plant exhibits increased resistance against said virus compared to a similar plant species without such TGB2 sequence.

2. (Currently Amended) The method Method according to the claim 1, wherein characterized in that the nucleotide sequence of the nucleotide construct has at least 80% homology with the nucleotide sequence of SEQ ID NO: 1, its complement or its corresponding RNA TGB2 of said virus or its complementary cDNA.

3. (Canceled)

4. (Currently Amended) The method Method according to claim 1, wherein characterized in that the plant cell is a stomatal cell.

5. (Currently Amended) The method Method according to claim 1, wherein ~~characterized in that~~ the plant is selected from the group consisting of sugar beet, potato, barley and ~~or~~ peanut.

6. (Currently Amended) The method Method according to claim 1, wherein ~~characterized in that~~ the virus is BNYVV, wherein the TGB2 ~~the~~ nucleotide sequence of TGB2 of said virus is comprised of SEQ ID NO: 3 and wherein the plant is *Beta vulgaris* ~~between the nucleotide 3287 and 3643 of the 5' strand of genomic or subgenomic RNA 2 of the BNYVV and the plant is a beet, preferably a sugar beet —~~ (*Beta vulgaris*).

7. (Currently Amended) The method Method according to claim 1, wherein ~~characterized in that~~ the regulatory sequence comprises a promoter sequence or a terminator sequence active in a plant.

8. (Currently Amended) The method Method according to claim 7, wherein ~~characterized in that~~ the promoter sequence is a ~~constitutive or~~ a foreigner promoter sequence.

9. (Currently Amended) The method Method according to ~~the preceding~~ claim 7, wherein ~~characterized in that~~ the promoter sequence is selected from the group consisting of 35S Cauliflower Mosaic Virus promoter; and/or the polyubiquitin *Arabidopsis thaliana* promoter.

10. (Currently Amended) The method Method according to claim 7, wherein ~~characterized in that~~ the promoter sequence is a promoter which is ~~capable of being~~ active mainly into the root tissues of plants, ~~such as the par promoter of the haemoglobin gene from Perosponia andersonii.~~

11. (Currently Amended) A transgenic Transgenic plant resistant to BNYVV, a group I virus comprising a nucleotide construct to express a TGB2 protein whose functional activity has been changed, the construct comprising having a nucleotide sequence at least 70% homology with homologous to the nucleotide sequence of SEQ ID NO: 1, its complement or its corresponding RNA, the sequence including at least one deletion, insertion, or substitution which

results in a mutant TGB2 protein being expressed which has at least one amino acid change compared to wild-type TBG2, of said virus sequence or its corresponding cDNA, being operably linked to one or more regulatory sequence(s) active in a plant.

12. (Currently Amended) The transgenic Transgenic plant according to the claim 11, wherein characterized in that the nucleotide construct has a nucleotide sequence corresponding to at least 80% homology with the nucleotide sequence of TGB2 of said virus or its complementary eDNA homologous to SEQ ID NO: 1, its complement or its corresponding RNA.

13. (Canceled)

14. (Currently Amended) The transgenic Transgenic plant according to claim 11 being a plant selected from the group consisting of sugar beet, potato, barley and or peanuts.

15. (Currently Amended) The transgenic Transgenic plant according to claim 11, wherein characterized in that the transgenic plant is being a beet, wherein preferably a sugar beet (*Beta vulgaris*) the virus is BNYVV and wherein the nucleotide sequence of TGB2 nucleotide sequence of said virus is comprised of a SEQ ID NO: 3, its complement or its corresponding RNA between the nucleotides 3287 and 3643 of the 5' strand of genomic or subgenomic RNA 2 of BNYVV or its corresponding cDNA.

16. (Currently Amended) The transgenic Transgenic plant according to the claim 11, wherein characterized in that the regulatory sequence comprises a promoter sequence and a terminator sequence active in a plant.

17. (Currently Amended) The transgenic Transgenic plant according to the claim 11, wherein characterized in that the regulatory sequence(s) comprise a promoter sequence which is a constitutive or a foreign promoter sequence.

18. (Currently Amended) The transgenic Transgenic plant according to the claim 17, wherein the characterized in that promoter sequence is selected from the group consisting of 35S

Cauliflower Mosaic Virus promoter; and/or the polyubiquitin *Arabidopsis thaliana* ~~*Arabidopsis thaliana*~~ promoter.

19. (Currently Amended) The transgenic Transgenic plant according to claim 17, ~~wherein the~~ characterized in that the promoter sequence is a promoter which is capable of being active mainly into root tissues, such as the par promoter of the haemoglobin gene from *Perosponia andersonii* ~~*Perosponia andersonii*~~ which is active mainly in root tissues.

20. (Currently Amended) The transgenic Transgenic plant according to claim 11, ~~wherein the plant~~ characterized in that it further carries natural tolerance to BNYVV Group I viruses.

21. (Currently Amended) The transgenic Transgenic plant according to claim 11, comprising at least one other type of resistance selected from the group consisting of ~~characterized in that it further comprises a pesticide, herbicide and or fungicide resistance, preferably a resistance selected from the group consisting of nematode resistance, glyphosate resistance, glufosomate resistance and/or acetochloride resistance.~~

22. (Currently Amended) A transgenic Transgenic plant tissue selected from the group consisting of fruit, stem, root, tuber, and seed of a plant according to claim 11.

23. (New) The method according to claim 1, wherein the homologous sequence is a variant sequence of SEQ ID NO:1 due to redundancy of code.

24. (New) The method according to claim 1, wherein a modification is made in the hydrophilic region of the wild-type sequence SEQ ID NO: 1 downstream of the N-terminal hydrophobic domain and just upstream of the conserved central domain.

25. (New) The method according to claim 24, wherein amino acids in said hydrophilic region are substituted by the amino acid alanine.

26. (New) The method according to claim 25, wherein the mutated nucleotide sequence is SEQ ID NO: 3.

27. (New) The transgenic plant according to claim 11, wherein the homologous sequence is a variant sequence of SEQ ID NO:1 due to redundancy of code.

28. (New) The transgenic plant according to claim 11, wherein a modification is made in the hydrophilic region of the wild-type sequence SEQ ID NO: 1 downstream of the N-terminal hydrophobic domain and just upstream of the conserved central domain.

29. (New) The transgenic plant according to claim 11, wherein amino acids in said hydrophilic region are substituted by the amino acid alanine.

30. (New) The transgenic plant according to claim 11, wherein the nucleotide sequence is SEQ ID NO: 3.

31. (New) The transgenic plant according to claim 15, wherein the transgenic plant is *Beta vulgaris*.

32. (New) The transgenic plant according to claim 21, wherein said at least one other type of resistance is selected from the group consisting of nematode resistance, glyphosate resistance, glufosinate resistance and acetochloride resistance.